

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.010G120100

Gene Model: Sobic.010G120100.1.p

Description: SbEXPB-42

Family: Beta Expansin

3D structure:



GENOME DATABASES

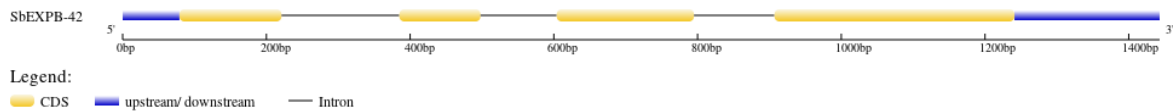
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

KEGG: <https://www.genome.jp/entry/T01086>

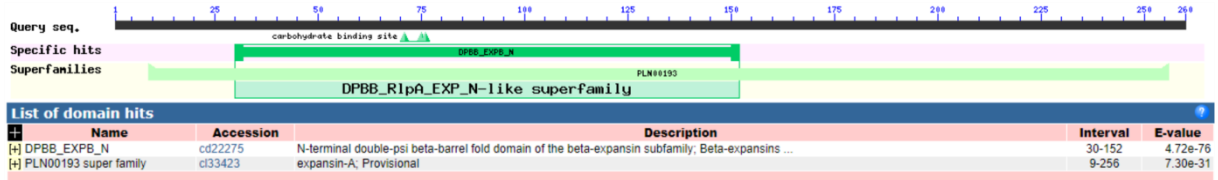
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPB-42

MACKQQIGVVVVLSCFIAISALAFRPCAAWSDAGATWYGPANGAGSDGGACGYQG
AVHQPPFSSMITAGSNSIYQDGKGCCTCYQVKCTGHQSCSGSPVTVVLTDQCPGACQ
SEPVHFDLSGTAFGAMAKPGQADQLRNVGRLPVQYTRVPCNWNGVDVAFRVDAGS
NANYLAMAIEYEAGDGLRAVELQNGAAAWAPMERSWGAVWRYQSSGSSLQAAP
LSVRLTSGSGKTLVASGVIPAGWQPGNTYRCVVNFGRN*

CDS (coding sequence)

>SbEXPB-42

ATGGCTTGCAAGCAGCAGATCGGGGTGGTCGTCGTCTTGTCTGCTTCATTGCCAT
CAGTGCTCTCGCCTTCCGTCCCTGCGCAGCCTGGTTCGGACGCCGGCGCCACCTGG
TACGGCCCTGCCAACGGCGCTGGGAGCGACGGTGGTGCCTGTGGGTACCAGGGT
GCCGTCCACCAGCCTCCGTTCTCGTCAATGATCACCGCCGGCAGCAATTCCATCT
ACCAGGACGGCAAGGGCTGCGGCACCTGCTACCAGGTGAAGTGCACCGGACACC
AGTCGTGCTCCGGCAGCCCGGTGACAGTGGTCCTCACTGACCAGTGCCCCGGCGC
TTGCCAGTCCGAGCCCGTCCACTTCGACCTCAGCGGGACGGCGTTCGGTGCCATG
GCGAAACCCGGCCAGGCCGACCAGTCCGAAACGTTCGGCCGCTCCCAGTCCAG
TACACCCGGGTGCCGTGCAACTGGAACGGCGTGGACGTGGCCTTCAGGGTGGAC
GCCGGCTCGAACGCCAACTACCTGGCCATGGCCATCGAGTACGAGGCCGGGGAC
GGGACCTGCGCGCCGTGGAGCTGCAAAATGGCGCGGGCGGGCGTGGGCGCCCATG
GAACGCTCCTGGGGCGCGGTGTGGCGCTACCAGTCGTCCGGCTCCAGTCTGCAGG
CGGCCCCCTGTCTGTCCGCCTCACCTCCGGCTCCGGCAAGACCCTCGTCGCCAG
CGGCGTCATCCCCGCCGATGGCAGCCCGGCAACACCTACCGCTGCGTCGTCAAC
TTCGGACGAAACTGA

Nucleotide

>SbEXPB-42

TCATTCTGTAGTAGTGCTAGTAGAACCCTCCTAGCTAGATCATTGGATACATAGTC
AGGCCAACAGATCGGCTTCCGGCATGGCTTGCAAGCAGCAGATCGGGGTGGTCG
TCGTCTTGTCTGCTTCATTGCCATCAGTGCTCTCGCCTTCCGTCCCTGCGCAGCCT

GGTCGGACGCCGGCGCCACCTGGTACGGCCCTGCCAACGGCGCTGGGAGCGACG
GTGCGTAAGTTCTCGTGTGTGTGCATTACCATGCATATGCATGTGTGTGTACACGT
TTTTTCATTGCGAATTCATCATATGCCTTTGCTATATACTATGATGATATGTAGAC
GTCAATGCATGCATGGTTAATCTATCTTTTTGTGGTATATACTACTGTAGGTGG
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GCCGGCAGCAATTCCATCTACCAGGACGGCAAGGGCTGCGGCACCTGCTACCAG
GTACGTCGATCAGGGTTACGTTTCATATATCTATCGGTTTCATGCAGTGCAAAGCGT
ATGCATCATGATCTTGTGTTGTTGTTGTACTIONACATATATACGTACTTCTCCAGGTGAA
GTGCACCGGACACCAGTCGTGCTCCGGCAGCCCGGTGACAGTGGTCTCTACTGAC
CAGTGCCCCGGCGCTTGCCAGTCCGAGCCCGTCCACTTCGACCTCAGCGGGACGG
CGTTCGGTGCCATGGCGAAACCCGGCCAGGCCGACCAGCTCCGAAACGTCGGCC
GCCTCCCAGTCCAGTACACCCGGTAAGTGATACTACATGCCTCTCACCGTCGATT
AGCTGCTTGCCCTGCACCGTCGTTCGTCCGTCCGTTCGTCATCGCAGCCGACGATCTG
ACCTGACTTGGCGCTGTCTGCAGGGTGCCGTGCAACTGGAACGGCGTGGACGTGG
CCTTCAGGGTGGACGCCGGCTCGAACGCCAACTACCTGGCCATGGCCATCGAGTA
CGAGGCCGGGGACGGGGACCTGCGCGCCGTGGAGCTGCAAAATGGCGCGGGCGGC
GTGGGCGCCATGGAACGCTCCTGGGGCGCGGTGTGGCGCTACCAGTCGTCCGGC
TCCAGTCTGCAGGCGGCCCCCTGTCTGTCCGCCTCACCTCCGGCTCCGGCAAGA
CCCTCGTCGCCAGCGGCGTCATCCCCGCCGGATGGCAGCCCGGCAACACCTACCG
CTGCGTCGTCAACTTCGGACGAACTGATACGAATGATATTATATTGCTACATTTT
CTACTCGTGTCTCAAATCCAATAAAATGCAGCATGCATGTGGCCTGCATGCTTGA
TCATATCCTCTGCTCTTCTTTGTGTCTGTTGATACTGACGATCAGCCAATGAACAG
TTGTGATCGGAACTCAACATGTGTAATGAAATGATACTCAACTAGAGAACATG
CATATCCC